I. AMENDMENTS TO THE CLAIMS

Claims 1 to 52. (Canceled)

Claim 53. (New) A method for detecting expression of a first transgenic nucleic acid molecule operably linked to a second transgenic nucleic acid molecule, wherein the second transgenic nucleic acid molecule is capable of producing an mRNA, the method comprising:

producing a complementary DNA from said mRNA;

amplifying the complementary DNA; and

detecting the complementary DNA by hybridization with at least one oligonucleotide designed to hybridize with the complementary DNA, wherein the hybridization indicates expression of the first transgenic nucleic acid molecule.

Claim 54. (New) The method according to claim 53, further comprising quantitation of mRNA transcribed from the second transgenic nucleic acid molecule.

Claim 55. (New) The method according to claim 53, wherein the second transgenic nucleic acid molecule is selected from the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences.

Claim 56. (New) The method according to claim 53, wherein the second transgenic nucleic acid molecule is a 3' untranslated sequence from the 3' end of the *Pisum sativum* rbcS E9 gene.

Claim 57. (New) The method according to claim 53, wherein the second transgenic nucleic acid molecule is SEQ ID NO: 2.

Claim 58. (New) The method according to claim 53, wherein the at least one oligonucleotide is a sequence which is a molecule selected from the group consisting of SEQ ID NO: 7 SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 28.

Claim 59. (New) The method according to claim 53, wherein the amplifying is carried out by a method selected from the group consisting of PCR or RT-PCR.

Claim 60. (New) The method according to claim 54, wherein the quantitation of mRNA is determined by a method selected from quantitative RT-PCR or competitive quantitative RT-PCR.

Claim 61. (New) The method according to claim 53, wherein the second transgenic nucleic acid molecule comprises at least 100 base pairs of consecutive sequence of SEQ ID NO: 2.

Claim 62. (New) The method according to claim 53, wherein at least one oligonucleotide comprises at least 15 bases from or complementary to a consecutive sequence of SEQ ID NO: 2.

Claim 63. (New) The method according to claim 53, wherein at least one oligonucleotide has a detectable label.

Claim 64. (New) The method according to claim 62, wherein the label is selected from the group consisting of a fluorescent label, a digoxigenen-dUTP label, a biotin label, and a radiolabel.

Claim 65. (New) The method according to claim 53, wherein the at least one oligonucleotide comprises a pair of oligonucleotide primers and an oligonucleotide probe designed to hybridize to the second transgenic nucleic acid molecule in a 5' nuclease assay.

Claim 66. (New) The method according to claim 64, wherein each of said primer pair used in the amplification comprises 15 to 30 bases identical or complementary to a consecutive sequence of a second transgenic nucleic acid molecule having a sequence selected from the group consisting of signal sequences, 3' UTR sequences, and 5' UTR sequences and wherein the probe comprises 15 to 30 bases complementary or identical to a second transgenic nucleic acid molecule having a sequence selected from the group consisting of signal sequences, 3' UTR sequences, and 5' UTR sequences.

Claim 67. (New) The method according to claim 53, further comprising Southern Blotting, Northern Blotting or RNAse protection assay.

Claim 68. (New) A method for detecting expression of a first transgenic nucleic acid molecule operably linked to a second transgenic nucleic acid molecule, wherein the second transgenic nucleic acid molecule is capable of producing an mRNA, the method comprising:

producing a complementary DNA from said mRNA;

amplifying the complementary DNA; and

detecting the complementary DNA by hybridization with at least one oligonucleotide designed to hybridize with the complementary DNA, wherein the hybridization indicates expression of the first transgenic nucleic acid molecule, and

wherein the at least one oligonucleotide is a sequence which is a molecule selected from the group consisting of SEQ ID NO: 7 SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 28.

Claim 69. (New) A method for detecting expression of a first transgenic nucleic acid molecule operably linked to a second transgenic nucleic acid molecule, wherein the second transgenic nucleic acid molecule is capable of producing an mRNA, the method comprising:

producing a complementary DNA from said mRNA;

amplifying the complementary DNA; and

detecting the complementary DNA by hybridization with at least one oligonucleotide designed to hybridize with the complementary DNA, wherein the hybridization indicates expression of the first transgenic nucleic acid molecule, and

wherein the second transgenic nucleic acid molecule is the sequence of SEQ ID NO: 2.